AMENDMENTS TO THE SPECIFICATION

At page 14, paragraph 1, lines 3-8, Applicants wish to correct obvious typographical errors and clarify that the amino acid positions are in reference to the positions provided in SEQ ID NO: 78. SEQ ID NO: 78 provides the 618 amino acid sequence of the human cIAP1 protein that is schematically presented in FIG. 5B. Applicants request replacement of paragraph 1, page 14 with the following paragraph:

> Fig. 5B shows a map of Omi cleavage sites on human cIAP1, the cIAP1 is labeled with the three mapped and unmapped sites, the three underlined amino acid sequences were the amino terminal sequences (determined by Edman Degradation) of the cleaved cIAP1 fragments F1/F2, F3 and F4, respectively, Omi cleaves cIAP1 (SEQ ID NO: 78) after the residue Thr4, Asn133, and Leu161 as denoted by the three arrows, both polypeptide fragments F1 and F2 start with the amino acid sequence ASQRLFPG, ~~F6 starts~~ F4 starts with SFAHSLSP, ~~and F5~~ and F3 with NSRAVEDI;

At page 21, paragraph 2, lines 12-13, Applicants wish to clarify that only SEQ ID NO. 14 represents the polypeptide that is inactive. Support for the amendment is provided at page 21, paragraph 2, lines 15-16 which states in relevant part "SEQ ID NOs. 15 and 16 are active Omi serine proteases...". Applicants request replacement of paragraph 2, page 21 with the following paragraph:

> The Omi WT nucleic acid sequence can be mutated so that the AVPS and PDZ nucleic acid sequence domains are eliminated. This is known as an Omi serine protease nucleic acid sequence, wherein the sequence is without PDZ and

AVPS domains. The hinge can also be removed. The Omi protease expresses a polypeptide that includes the triad and associated residue chains. SEQ ID NOs. 14-16 are Omi with the AVPS removed, as well as a mutation of other parts of the sequence resulting in an inactive polypeptide (SEQ ID NO. 14). SEQ ID NO. 14 is the Omi serine protease nucleic acid sequence with AVPS and PDZ removed. Additionally, the catalytic triad can be altered or substituted concurrent with the removal of AVPS & PDZ. SEQ ID NOs. 15 and 16 are active Omi serine protease sequences with substitutions in the triad.

At page 33, lines 21-22, delete the phrase "and two residues, which form part of the residue chains". The phrase was inadvertently included and refers to SEQ ID NO. 70 as supported on page 34, lines 5-6 of the Specification. Further support for the amendment is found in the Sequence Listing, which shows that SEQ ID NO. 60 includes the two referenced residues. Applicants request replacement of paragraph 5, page 20 (lines 20-21), which continues onto the top of page 34, lines 1-2 with the following paragraph:

Finally, the Omi WT sequence can be of a short form, SEQ ID NO. 60 is an active sequence that does not include the hinge, PDZ, and AVPS~~, and two residues, which form part of the residue chains~~. The triad in SEQ ID NO. 60 is not substituted; however, SEQ ID NO. 61 is short, active, and has substitutions in the triad. SEQ ID NOs. 62 and 63 are short, active enzymes. SEQ ID NOs. 64 and 65 are short, inactive enzymes.

At page 34, paragraph 1, Applicants wish to clarify that the referenced active sequences are SEQ ID NOs. 66-69 and do not include SEQ ID NO. 65. SEQ ID NO. 65 is clearly identified

as being inactive. See p. 34, line 2. Applicants request replacement of paragraph 1, page 34 with the following paragraph:

> SEQ ID NOs. 65-69 have the hinge and PDZ removed. Residues within the sequence are removed from the residue chains. The sequences (SEQ ID NOs. 66-69) are active, but have nucleotides, which encode residue chains deleted. SEQ ID NO. 70 has AVPS, the hinge, and PDZ removed along with two residues at the end. SEQ ID NOs. 71-75 are the same, but with triad additions or alterations.

Finally, beginning at p. 37, paragraph 4 (lines 22-23) and continuing onto p. 38 (lines 1-16), Applicants wish to correct a typographical error regarding the referenced amino acid positions of SEQ ID NO. 60. As evidenced by the Sequence Listing, SEQ ID NO. 60 is 208 amino acids in length and not 529 amino acids as indicated in the text. Applicants request replacement of paragraph 4, page 37, which continues onto page 38, with the following paragraph:

> Thus, the Omi WT or recombinase polypeptide, as expressed in the cells in which it is normally expressed or in other eukaryotic cells, has a molecular weight of about 57 kDa, as estimated from the nucleic acid sequence SEQ ID NO. 1. The recombinant Omi polypeptide has one or more of the following characteristics:
>
> (i) it is approximately 529 amino acids in length;
>
> (ii) it has the ability to cleave a substrate, e.g., a protein;

(iii) it has a molecular weight, amino acid composition or other physical characteristic of SEQ ID NO. 44;

(iv) it has an overall sequence similarity of at least 50%, preferably at least 60%, more preferably at least 70%, 80%, 90%, or 95%, with SEQ ID NO. 44;

(v) it is found in all human tissues;

(vi) it has at least one PDZ domain, which is preferably about 70%, 80%, 90%, or 95% identical to SEQ ID NO. 76;

(vii) it has an AVPS domain, which is preferably about 70%, 80%, 90%, or 95% identical to SEQ ID NO. 77; and,

(viii) it has a carboxy terminal serine protease catalytic domain containing at least one site of serine protease activity, which is preferably about 70%, 80%, 90%, or 95% identical to amino acid residues ~~181–529~~ 1-208 of SEQ ID NO. 60.

This amendment introduces no new matter and is made solely to correct obvious typographical errors and clarify the meaning of the reference sequences as supported by the Specification, Drawings, and Sequence Listing.